

RAW SEQUENCE LISTING

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Application Serial Number: 10/562,324A
Source: IFWP
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IFWP

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DATE: 03/16/2007

PATENT APPLICATION: US/10/562,324A

TIME: 11:00:13

Input Set : A:\LeA 36 695.ST25.txt

Output Set: N:\CRF4\03162007\J562324A.raw

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3 <110> APPLICANT: Bayer HealthCare AG
4     Greif, Gisela
5     Hosse, Ralf
6     Krucken, Jurgen
7     Wunderlich, Frank
9 <120> TITLE OF INVENTION: Use of Novel Eimeria Gene and Corresponding Protein
11 <130> FILE REFERENCE: LeA 36 695
13 <140> CURRENT APPLICATION NUMBER: US 10/562,324A
14 <141> CURRENT FILING DATE: 2005-12-23
16 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/007080
17 <151> PRIOR FILING DATE: 2004-06-30
19 <150> PRIOR APPLICATION NUMBER: DE10330235.2
20 <151> PRIOR FILING DATE: 2003-07-04
22 <160> NUMBER OF SEQ ID NOS: 24
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1186
28 <212> TYPE: DNA
29 <213> ORGANISM: Eimeria tenella
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (83)..(679)
36 <400> SEQUENCE: 1
37 caggacccca aaataaaatc aaaggctatc acactatctt acttcttaac cgtttactga      60
39 ggctacaaga acaagtttga ag atg agg act atc cta gcc acc cta gtc ggt      112
40                               Met Arg Thr Ile Leu Ala Thr Leu Val Gly
41                               1           5           10
43 ttc aca gcc tgc gca gcc gtt gct gca gac gga gca cct gag tat cct      160
44 Phe Thr Ala Cys Ala Ala Val Ala Ala Asp Gly Ala Pro Glu Tyr Pro
45           15           20           25
47 tct cag ctt gca gtt gaa atc gat cca gaa gcg att att gcg atc cag      208
48 Ser Gln Leu Ala Val Glu Ile Asp Pro Glu Ala Ile Ile Ala Ile Gln
49           30           35           40
51 caa gat gca aac gcc gac cca cgt ctc ttt ttc cca ctg agc ggg ctt      256
52 Gln Asp Ala Asn Ala Asp Pro Arg Leu Phe Phe Pro Leu Ser Gly Leu
53           45           50           55
55 gtc tcc gcc aaa ctt gcc aaa gtc ttt caa ccc aac ata tac cca acc      304
56 Val Ser Ala Lys Leu Ala Lys Val Phe Gln Pro Asn Ile Tyr Pro Thr
57           60           65           70
59 cct cct agt ccc cag aca act tac cac ttt cac ctc cat cct cat ccc      352
60 Pro Pro Ser Pro Gln Thr Thr Tyr His Phe His Leu His Pro His Pro
61 75           80           85           90
63 cat tat ccg cat cct cag cca agt tat cct cat cct caa ccc cat cat      400

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64 His Tyr Pro His Pro Gln Pro Ser Tyr Pro His Pro Gln Pro His His
65          95          100          105
67 cct cat cct cat cct tat cat cct cat cct cat ccc cat cat cct cat      448
68 Pro His Pro His Pro Tyr His Pro His Pro His Pro His His Pro His
69          110          115          120
71 cct cat ccc cat caa cat cct cat cgt cat ccc gac cat cat ccc cac      496
72 Pro His Pro His Gln His Pro His Arg His Pro Asp His His Pro His
73          125          130          135
75 cat cat cct cac cat cat cat cat gaa cat aat gtt cat gtg cct caa      544
76 His His Pro His His His His His His Glu His Asn Val His Val Pro Gln
77          140          145          150
79 cat cag cac gct caa cac aac ggc cac cag aac aac ggt ggc cca gct      592
80 His Gln His Ala Gln His Asn Gly His Gln Asn Asn Gly Gly Pro Ala
81 155          160          165          170
83 cat tat cac cat gac tac cat ttt gcg cat cct cat caa gag aac cag      640
84 His Tyr His His Asp Tyr His Phe Ala His Pro His Gln Glu Asn Gln
85          175          180          185
87 cat cac cgc gag gaa gag cag ctt acc gac atc aac taa gctattggtc      689
88 His His Arg Glu Glu Glu Gln Leu Thr Asp Ile Asn
89          190          195
91 gggaattaag gtgcttagtc tcagtagtca gtacagtact aggctacgtc tgagatcttc      749
93 atggcaaaga ggtaccagcc accaagctga ctcggtatg ttttattaga caaatataaa      809
95 tttaaagggt cccagtttca gtctctgcag gtctgccct gaaagcacga gaggggccta      869
97 aagggtgatt ggagctgcaa atacagctgc aaatgcagct gcaaagtgcc gcttcaaaaa      929
99 agggacaggc ttcccgccaa aatttttggga tcatacctat caatgcttcg agaaaacata      989
101 gaaaacaaaa gcaactgaaga acgttcatag tcggtagttt taggggcatg ccgtgtgcta      1049
103 aaatcccatc gaaccttcag gtacacctga tcgttacgaa gtacacacca ccggtcactc      1109
105 tcaacgcgca ccaactagagc gagagctgct tcagggatgc agcgagatgt cgactcagag      1169
107 gtcctacatt aaaggga      1186
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112 <212> TYPE: PRT
113 <213> ORGANISM: Eimeria tenella
115 <400> SEQUENCE: 2
117 Met Arg Thr Ile Leu Ala Thr Leu Val Gly Phe Thr Ala Cys Ala Ala
118 1          5          10          15
121 Val Ala Ala Asp Gly Ala Pro Glu Tyr Pro Ser Gln Leu Ala Val Glu
122          20          25          30
125 Ile Asp Pro Glu Ala Ile Ile Ala Ile Gln Gln Asp Ala Asn Ala Asp
126          35          40          45
129 Pro Arg Leu Phe Phe Pro Leu Ser Gly Leu Val Ser Ala Lys Leu Ala
130          50          55          60
133 Lys Val Phe Gln Pro Asn Ile Tyr Pro Thr Pro Pro Ser Pro Gln Thr
134 65          70          75          80
137 Thr Tyr His Phe His Leu His Pro His Pro His Tyr Pro His Pro Gln
138          85          90          95
141 Pro Ser Tyr Pro His Pro Gln Pro His His Pro His Pro His Pro Tyr
142          100          105          110
145 His Pro His Pro His Pro His His Pro His Pro His Pro His Gln His

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146          115          120          125
149 Pro His Arg His Pro Asp His His Pro His His His Pro His His His
150          130          135          140
153 His His Glu His Asn Val His Val Pro Gln His Gln His Ala Gln His
154 145          150          155          160
157 Asn Gly His Gln Asn Asn Gly Gly Pro Ala His Tyr His His Asp Tyr
158          165          170          175
161 His Phe Ala His Pro His Gln Glu Asn Gln His His Arg Glu Glu Glu
162          180          185          190
165 Gln Leu Thr Asp Ile Asn
166          195
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 597
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172 <213> ORGANISM: Eimeria tenella
174 <400> SEQUENCE: 3
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177 ggagcacctg agtatccttc tcagcttgca gttgaaatcg atccagaagc gattattgcg      120
179 atccagcaag atgcaaacgc cgacccacgt ctctttttcc cactgagcgg gcttgtctcc      180
181 gccaaacttg ccaaagtctt tcaacccaac atatacccaa cccctcctag tccccagaca      240
183 acttaccact ttcacctcca tctcatccc cattatccgc atcctcagcc aagttatcct      300
185 catcctcaac cccatcatcc tcatcctcat ccttatcatc ctcatcctca tccccatcat      360
187 cctcatcctc atccccatca acatcctcat cgtcatcccg accatcatcc ccaccatcat      420
189 cctcaccatc atcatcatga acataatgtt catgtgcctc aacatcagca cgctcaacac      480
191 aacggccacc agaacaacgg tggcccagct cattatcacc atgactacca ttttgcgcat      540
193 cctcatcaag agaaccagca tcaccgcgag gaagagcagc ttaccgacat caactaa      597
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 25
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Primer A17-22-up
204 <400> SEQUENCE: 4
205 tctcatcct tatcatcctc atcct      25
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 18
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Primer A17-112-lo
216 <400> SEQUENCE: 5
217 gtggggatga tggtcggg      18
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 33
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Primer A17-f-length-64-up
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229 caggacccca aaataaaatc aaaggctatc aca 33
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234 <212> TYPE: DNA
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238 <223> OTHER INFORMATION: Primer A17-f-length-1176-lo
240 <400> SEQUENCE: 7
241 tgaccggtgg tgtgtacttc gtaac 25
244 <210> SEQ ID NO: 8
245 <211> LENGTH: 25
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
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252 <400> SEQUENCE: 8
253 ctgtgagaag aaccgggtgc tcttc 25
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257 <211> LENGTH: 24
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Primer EtACTIN-lo
264 <400> SEQUENCE: 9
265 cgtgcgaaaa tgccggacga agag 24
268 <210> SEQ ID NO: 10
269 <211> LENGTH: 32
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Primer A17-max-90-up
276 <400> SEQUENCE: 10
277 tgaggactat cctagccacc ctagtcggtt tc 32
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281 <211> LENGTH: 32
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Primer A17-max-150-up
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292 <210> SEQ ID NO: 12
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294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Primer A17-max-533-lo
300 <400> SEQUENCE: 12
301 tatgttcacg atgatgatgg tgaggatgat gg 32

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Input Set : A:\LeA 36 695.ST25.txt

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309 <220> FEATURE:
310 <223> OTHER INFORMATION: Primer A17-max-631-lo
312 <400> SEQUENCE: 13
313 aggatgcgca aaatggtagt catggtgata at 32
316 <210> SEQ ID NO: 14
317 <211> LENGTH: 27
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Primer pG8SAET-up
324 <400> SEQUENCE: 14
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328 <210> SEQ ID NO: 15
329 <211> LENGTH: 27
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Primer pG8SAET-lo
336 <400> SEQUENCE: 15
337 cgatatattc ggtcgctgag gcttgca 27
340 <210> SEQ ID NO: 16
341 <211> LENGTH: 27
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Primer pG8SAET-seq-up-140
348 <400> SEQUENCE: 16
349 atgatgactt tacaaataca tacaggg 27
352 <210> SEQ ID NO: 17
353 <211> LENGTH: 32
354 <212> TYPE: DNA
355 <213> ORGANISM: Artificial Sequence
357 <220> FEATURE:
358 <223> OTHER INFORMATION: Primer A17-sequent-27-up
360 <400> SEQUENCE: 17
361 cgaggaagag cagcttaccg acatcaacta ag 32
364 <210> SEQ ID NO: 18
365 <211> LENGTH: 32
366 <212> TYPE: DNA
367 <213> ORGANISM: Artificial Sequence
369 <220> FEATURE:
370 <223> OTHER INFORMATION: Primer A17-sequent-44-up
372 <400> SEQUENCE: 18
373 ccgacatcaa ctaagctatt ggtcgggaat ta 32
376 <210> SEQ ID NO: 19

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VERIFICATION SUMMARY

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